



## SEQUENCE LISTING

<110> ALBANI, SALVATORE

<120> METHOD FOR ISOLATION, QUANTIFICATION, CHARACTERIZATION  
AND MODULATION OF ANTIGEN-SPECIFIC T' CELLS

<130> AND-TCCCIPI1-DIV2

<140> 10/617,639

<141> 2003-07-07

<150> 09/756,983

<151> 2001-01-09

<150> PCT/US99/24666

<151> 1999-10-19

<150> 09/421,506

<151> 1999-10-19

<150> 60/105,018

<151> 1998-10-20

<160> 24

<170> PatentIn Ver. 2.1

<210> 1

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide derived  
from third hyper V region of IE molecule of Mus musculus

<400> 1

Ala Ser Phe Glu Ala Gln Gly Ala Leu Ala Asn Ile Ala Val Asp Lys  
1 5 10 15

Ala

<210> 2

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide derived  
from bole I protein of Epstein Barr virus

<400> 2

Thr Arg Asp Asp Ala Glu Tyr Leu Leu Gly Arg Glu Ser Val Leu  
1 5 10 15

<210> 3  
 <211> 16  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic peptide derived  
 from the haemophilus influenza virus

<400> 3  
 Thr Ser Phe Pro Met Arg Gly Asp Leu Ala Lys Arg Glu Pro Asp Lys  
           1                  5                  10                  15

<210> 4  
 <211> 36  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic peptide derived  
 from the TCR receptor of Mus musculus

<220>  
 <221> MOD\_RES  
 <222> (18)  
 <223> Ser, Ile or Thr

<400> 4  
 Leu His Ile Ser Ala Val Asp Pro Glu Asp Ser Ala Val Tyr Phe Cys  
           1                  5                  10                  15

Ala Xaa Ser Gln Glu Phe Phe Ser Ser Tyr Glu Gln Tyr Phe Gly Pro  
                   20                  25                  30

Gly Thr Arg Leu  
                   35

<210> 5  
 <211> 9  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic peptide derived  
 from the influenza virus

<400> 5  
 Gly Ile Leu Gly Phe Val Phe Thr Leu  
           1                  5

<210> 6  
 <211> 9

<212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic peptide derived  
 from the influenza virus

<400> 6  
 Val Lys Leu Gly Glu Phe Tyr Asn Gln  
 1 5

<210> 7  
 <211> 11  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic peptide

<220>  
 <221> MOD\_RES  
 <222> (2)  
 <223> cyclohexylalanine

<400> 7  
 Lys Xaa Val Ala Ala Trp Thr Leu Lys Ala Ala  
 1 5 10

<210> 8  
 <211> 13  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic peptide derived  
 from the influenza virus

<400> 8  
 Pro Lys Tyr Val Lys Gln Asn Thr Leu Lys Leu Ala Thr  
 1 5 10

<210> 9  
 <211> 17  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic peptide

<400> 9  
 Ile Ser Gln Ala Val His Ala Ala His Ala Glu Ile Asn Glu Ala Gly  
 1 5 10 15

Arg

<210> 10  
 <211> 15  
 <212> PRT  
 <213> Escherichia coli

<400> 10  
 Gln Lys Arg Ala Ala Tyr Asp Gln Tyr Gly His Ala Ala Phe Glu  
     1                    5                    10                    15

<210> 11  
 <211> 15  
 <212> PRT  
 <213> Homo sapiens

<400> 11  
 Gln Lys Arg Ala Ala Val Asp Thr Tyr Cys Arg His Asn Tyr Gly  
     1                    5                    10                    15

<210> 12  
 <211> 9  
 <212> PRT  
 <213> Homo sapiens

<400> 12  
 Gly Ile Leu Gly Phe Val Phe Thr Leu  
     1                    5

<210> 13  
 <211> 9  
 <212> PRT  
 <213> Homo sapiens

<400> 13  
 Val Lys Leu Gly Glu Phe Tyr Asn Gln  
     1                    5

<210> 14  
 <211> 13  
 <212> PRT  
 <213> Homo sapiens

<400> 14  
 Pro Lys Tyr Val Lys Gln Asn Thr Leu Lys Leu Ala Thr  
     1                    5                    10

<210> 15  
 <211> 942  
 <212> DNA  
 <213> Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: Fusion construct with human and bacterial sequences

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(939)

&lt;400&gt; 15

atg ggc cac aca cgg agg cag gga aca tca cca tcc aag tgt cca tac	48
Met Gly His Thr Arg Arg Gln Gly Thr Ser Pro Ser Lys Cys Pro Tyr	
1 5 10 15	
ctc aat ttc ttt cag ctc ttg gtg ctg gct ggt ctt tct cac ttc tgt	96
Leu Asn Phe Phe Gln Leu Leu Val Leu Ala Gly Leu Ser His Phe Cys	
20 25 30	
tca ggt gtt atc cac gtg acc aag gaa gtg aaa gaa gtg gca acg ctg	144
Ser Gly Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu	
35 40 45	
tcc tgt ggt cac aat gtt tct gtt gaa gag ctg gca caa act cgc atc	192
Ser Cys Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile	
50 55 60	
tac tgg caa aag gag aag aaa atg gtg ctg act atg atg tct ggg gac	240
Tyr Trp Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp	
65 70 75 80	
atg aat ata tgg ccc gag tac aag aac cgg acc atc ttt gat atc act	288
Met Asn Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr	
85 90 95	
aat aac ctc tcc att gtg atc ctg gct ctg cgc cca tct gac gag ggc	336
Asn Asn Leu Ser Ile Val Ile Leu Ala Leu Arg Pro Ser Asp Glu Gly	
100 105 110	
aca tac gag tgt gtt gtt ctg aag tat gaa aaa gac gct ttc aag cgg	384
Thr Tyr Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg	
115 120 125	
gaa cac ctg gct gaa gtg acg tta tca gtc aaa gct gac ttc cct aca	432
Glu His Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp Phe Pro Thr	
130 135 140	
cct agt ata tct gac ttt gaa att cca act tct aat att aga agg ata	480
Pro Ser Ile Ser Asp Phe Glu Ile Pro Thr Ser Asn Ile Arg Arg Ile	
145 150 155 160	
att tgc tca acc tct gga ggt ttt cca gag cct cac ctc tcc tgg ttg	528
Ile Cys Ser Thr Ser Gly Gly Phe Pro Glu Pro His Leu Ser Trp Leu	
165 170 175	
gaa aat gga gaa gaa tta aat gcc atc aac aca aca gtt tcc caa gat	576
Glu Asn Gly Glu Glu Leu Asn Ala Ile Asn Thr Thr Val Ser Gln Asp	
180 185 190	

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cct gaa act gag ctc tat gct gtt agc gaa ttc ggc ggc tcc ggt ggt 624
Pro Glu Thr Glu Leu Tyr Ala Val Ser Glu Phe Gly Gly Ser Gly Gly
      195                      200                      205

agc gcc aca cct caa aat att act gat ttg tgt gca gaa tac cac aac 672
Ser Ala Thr Pro Gln Asn Ile Thr Asp Leu Cys Ala Glu Tyr His Asn
      210                      215                      220

aca caa ata cat acg cta aat gat aag ata ttt tcg tat aca gaa tct 720
Thr Gln Ile His Thr Leu Asn Asp Lys Ile Phe Ser Tyr Thr Glu Ser
      225                      230                      235                      240

cta gct gga aaa aga gag atg gct atc att act ttt aag aat ggt gca 768
Leu Ala Gly Lys Arg Glu Met Ala Ile Ile Thr Phe Lys Asn Gly Ala
      245                      250                      255

act ttt caa gta gaa gta cca ggt agt caa cat ata gat tca caa aaa 816
Thr Phe Gln Val Glu Val Pro Gly Ser Gln His Ile Asp Ser Gln Lys
      260                      265                      270

aaa gcg att gaa agg atg aag gat acc ctg agg att gca tat ctt act 864
Lys Ala Ile Glu Arg Met Lys Asp Thr Leu Arg Ile Ala Tyr Leu Thr
      275                      280                      285

gaa gct aaa gtc gaa aag tta tgt gta tgg aat aat aaa acg cct cat 912
Glu Ala Lys Val Glu Lys Leu Cys Val Trp Asn Asn Lys Thr Pro His
      290                      295                      300

gcg att gcc gca att agt atg gca aat taa 942
Ala Ile Ala Ala Ile Ser Met Ala Asn
      305                      310

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<210> 16

<211> 313

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fusion construct with human and bacterial sequences

<400> 16

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Met Gly His Thr Arg Arg Gln Gly Thr Ser Pro Ser Lys Cys Pro Tyr
  1                      5                      10                      15

Leu Asn Phe Phe Gln Leu Leu Val Leu Ala Gly Leu Ser His Phe Cys
      20                      25                      30

Ser Gly Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu
      35                      40                      45

Ser Cys Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile
      50                      55                      60

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Tyr Trp Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp  
 65 70 75 80  
 Met Asn Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr  
 85 90 95  
 Asn Asn Leu Ser Ile Val Ile Leu Ala Leu Arg Pro Ser Asp Glu Gly  
 100 105 110  
 Thr Tyr Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg  
 115 120 125  
 Glu His Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp Phe Pro Thr  
 130 135 140  
 Pro Ser Ile Ser Asp Phe Glu Ile Pro Thr Ser Asn Ile Arg Arg Ile  
 145 150 155 160  
 Ile Cys Ser Thr Ser Gly Gly Phe Pro Glu Pro His Leu Ser Trp Leu  
 165 170 175  
 Glu Asn Gly Glu Glu Leu Asn Ala Ile Asn Thr Thr Val Ser Gln Asp  
 180 185 190  
 Pro Glu Thr Glu Leu Tyr Ala Val Ser Glu Phe Gly Gly Ser Gly Gly  
 195 200 205  
 Ser Ala Thr Pro Gln Asn Ile Thr Asp Leu Cys Ala Glu Tyr His Asn  
 210 215 220  
 Thr Gln Ile His Thr Leu Asn Asp Lys Ile Phe Ser Tyr Thr Glu Ser  
 225 230 235 240  
 Leu Ala Gly Lys Arg Glu Met Ala Ile Ile Thr Phe Lys Asn Gly Ala  
 245 250 255  
 Thr Phe Gln Val Glu Val Pro Gly Ser Gln His Ile Asp Ser Gln Lys  
 260 265 270  
 Lys Ala Ile Glu Arg Met Lys Asp Thr Leu Arg Ile Ala Tyr Leu Thr  
 275 280 285  
 Glu Ala Lys Val Glu Lys Leu Cys Val Trp Asn Asn Lys Thr Pro His  
 290 295 300  
 Ala Ile Ala Ala Ile Ser Met Ala Asn  
 305 310

<210> 17

<211> 1056

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fusion construct with

## human and bacterial sequences

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(1053)

&lt;400&gt; 17

atg gga ctg agt aac att ctc ttt gtg atg gcc ttc ctg ctc tct ggt	48
Met Gly Leu Ser Asn Ile Leu Phe Val Met Ala Phe Leu Leu Ser Gly	
1 5 10 15	
gct gct cct ctg aag att caa gct tat ttc aat gag act gca gac ctg	96
Ala Ala Pro Leu Lys Ile Gln Ala Tyr Phe Asn Glu Thr Ala Asp Leu	
20 25 30	
cca tgc caa ttt gca aac tct caa aac caa agc ctg agt gag cta gta	144
Pro Cys Gln Phe Ala Asn Ser Gln Asn Gln Ser Leu Ser Glu Leu Val	
35 40 45	
gta ttt tgg cag gac cag gaa aac ttg gtt ctg aat gag gta tac tta	192
Val Phe Trp Gln Asp Gln Glu Asn Leu Val Leu Asn Glu Val Tyr Leu	
50 55 60	
ggc aaa gag aaa ttt gac agt gtt cat tcc aag tat atg ggc cgc aca	240
Gly Lys Glu Lys Phe Asp Ser Val His Ser Lys Tyr Met Gly Arg Thr	
65 70 75 80	
agt ttt gat tcg gac agt tgg acc ctg aga ctt cac aat ctt cag atc	288
Ser Phe Asp Ser Asp Ser Trp Thr Leu Arg Leu His Asn Leu Gln Ile	
85 90 95	
aag gac aag ggc ttg tat caa tgt atc atc cat cac aaa aag ccc aca	336
Lys Asp Lys Gly Leu Tyr Gln Cys Ile Ile His His Lys Lys Pro Thr	
100 105 110	
gga atg att cgc atc cac cag atg aat tct gaa ctg tca gtg ctt gct	384
Gly Met Ile Arg Ile His Gln Met Asn Ser Glu Leu Ser Val Leu Ala	
115 120 125	
aac ttc agt caa cct gaa ata gta cca att tct aat ata aca gaa aat	432
Asn Phe Ser Gln Pro Glu Ile Val Pro Ile Ser Asn Ile Thr Glu Asn	
130 135 140	
gtg tac ata aat ttg acc tgc tca tct ata cac ggt tac cca gaa cct	480
Val Tyr Ile Asn Leu Thr Cys Ser Ser Ile His Gly Tyr Pro Glu Pro	
145 150 155 160	
aag aag atg agt gtt ttg cta aga acc aag aat tca act atc gag tat	528
Lys Lys Met Ser Val Leu Leu Arg Thr Lys Asn Ser Thr Ile Glu Tyr	
165 170 175	
gat ggt att atg cag aaa tct caa gat aat gtc aca gaa ctg tac gac	576
Asp Gly Ile Met Gln Lys Ser Gln Asp Asn Val Thr Glu Leu Tyr Asp	
180 185 190	



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gtt tcc atc agc ttg tct gtt tca ttc cct gat gtt acg agc aat atg 624
Val Ser Ile Ser Leu Ser Val Ser Phe Pro Asp Val Thr Ser Asn Met
      195                200                205

acc atc ttc tgt att ctg gaa act gac aag acg cgg ctt tta tct tca 672
Thr Ile Phe Cys Ile Leu Glu Thr Asp Lys Thr Arg Leu Leu Ser Ser
      210                215                220

cct ttc tct ata gag ctt gag gac cct cag cct ccc cca gac cac gaa 720
Pro Phe Ser Ile Glu Leu Glu Asp Pro Gln Pro Pro Pro Asp His Glu
      225                230                235                240

ttc ggc ggc tcc ggt ggt agc gcc aca cct caa aat att act gat ttg 768
Phe Gly Gly Ser Gly Gly Ser Ala Thr Pro Gln Asn Ile Thr Asp Leu
      245                250                255

tgt gca gaa tac cac aac aca caa ata cat acg cta aat gat aag ata 816
Cys Ala Glu Tyr His Asn Thr Gln Ile His Thr Leu Asn Asp Lys Ile
      260                265                270

ttt tcg tat aca gaa tct cta gct gga aaa aga gag atg gct atc att 864
Phe Ser Tyr Thr Glu Ser Leu Ala Gly Lys Arg Glu Met Ala Ile Ile
      275                280                285

act ttt aag aat ggt gca act ttt caa gta gaa gta cca ggt agt caa 912
Thr Phe Lys Asn Gly Ala Thr Phe Gln Val Glu Val Pro Gly Ser Gln
      290                295                300

cat ata gat tca caa aaa aaa gcg att gaa agg atg aag gat acc ctg 960
His Ile Asp Ser Gln Lys Lys Ala Ile Glu Arg Met Lys Asp Thr Leu
      305                310                315                320

agg att gca tat ctt act gaa gct aaa gtc gaa aag tta tgt gta tgg 1008
Arg Ile Ala Tyr Leu Thr Glu Ala Lys Val Glu Lys Leu Cys Val Trp
      325                330                335

aat aat aaa acg cct cat gcg att gcc gca att agt atg gca aat taa 1056
Asn Asn Lys Thr Pro His Ala Ile Ala Ala Ile Ser Met Ala Asn
      340                345                350

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<210> 18

<211> 351

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fusion construct with human and bacterial sequences

<400> 18

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Met Gly Leu Ser Asn Ile Leu Phe Val Met Ala Phe Leu Leu Ser Gly
  1              5              10              15

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Ala Ala Pro Leu Lys Ile Gln Ala Tyr Phe Asn Glu Thr Ala Asp Leu
      20              25              30

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Pro Cys Gln Phe Ala Asn Ser Gln Asn Gln Ser Leu Ser Glu Leu Val  
 35 40 45  
 Val Phe Trp Gln Asp Gln Glu Asn Leu Val Leu Asn Glu Val Tyr Leu  
 50 55 60  
 Gly Lys Glu Lys Phe Asp Ser Val His Ser Lys Tyr Met Gly Arg Thr  
 65 70 75 80  
 Ser Phe Asp Ser Asp Ser Trp Thr Leu Arg Leu His Asn Leu Gln Ile  
 85 90 95  
 Lys Asp Lys Gly Leu Tyr Gln Cys Ile Ile His His Lys Lys Pro Thr  
 100 105 110  
 Gly Met Ile Arg Ile His Gln Met Asn Ser Glu Leu Ser Val Leu Ala  
 115 120 125  
 Asn Phe Ser Gln Pro Glu Ile Val Pro Ile Ser Asn Ile Thr Glu Asn  
 130 135 140  
 Val Tyr Ile Asn Leu Thr Cys Ser Ser Ile His Gly Tyr Pro Glu Pro  
 145 150 155 160  
 Lys Lys Met Ser Val Leu Leu Arg Thr Lys Asn Ser Thr Ile Glu Tyr  
 165 170 175  
 Asp Gly Ile Met Gln Lys Ser Gln Asp Asn Val Thr Glu Leu Tyr Asp  
 180 185 190  
 Val Ser Ile Ser Leu Ser Val Ser Phe Pro Asp Val Thr Ser Asn Met  
 195 200 205  
 Thr Ile Phe Cys Ile Leu Glu Thr Asp Lys Thr Arg Leu Leu Ser Ser  
 210 215 220  
 Pro Phe Ser Ile Glu Leu Glu Asp Pro Gln Pro Pro Pro Asp His Glu  
 225 230 235 240  
 Phe Gly Gly Ser Gly Gly Ser Ala Thr Pro Gln Asn Ile Thr Asp Leu  
 245 250 255  
 Cys Ala Glu Tyr His Asn Thr Gln Ile His Thr Leu Asn Asp Lys Ile  
 260 265 270  
 Phe Ser Tyr Thr Glu Ser Leu Ala Gly Lys Arg Glu Met Ala Ile Ile  
 275 280 285  
 Thr Phe Lys Asn Gly Ala Thr Phe Gln Val Glu Val Pro Gly Ser Gln  
 290 295 300  
 His Ile Asp Ser Gln Lys Lys Ala Ile Glu Arg Met Lys Asp Thr Leu  
 305 310 315 320  
 Arg Ile Ala Tyr Leu Thr Glu Ala Lys Val Glu Lys Leu Cys Val Trp  
 325 330 335

Asn Asn Lys Thr Pro His Ala Ile Ala Ala Ile Ser Met Ala Asn  
340 345 350

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<210> 19
<211> 31
<212> PRT
<213> Artificial Sequence
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<220>
<223> Description of Artificial Sequence: Synthetic peptide
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<400> 19  
Ser Ala Gln Leu Glu Trp Glu Leu Gln Ala Leu Glu Lys Glu Asn Ala  
1 5 10 15  
Gln Leu Glu Trp Glu Leu Gln Ala Leu Glu Lys Glu Leu Ala Gln  
20 25 30

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<210> 20
<211> 30
<212> PRT
<213> Artificial Sequence
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<220>  
<223> Description of Artificial Sequence: Synthetic peptide

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<400> 20
Ala Gln Leu Lys Lys Lys Leu Gln Ala Leu Lys Lys Lys Asn Ala Gln
  1             5             10             15

Leu Lys Gln Lys Leu Gln Ala Leu Lys Lys Lys Leu Ala Gln
      20             25             30

```

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<210> 21
<211> 1095
<212> DNA
<213> Artificial Sequence
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<220>  
<223> Description of Artificial Sequence: Fusion construct with human and bacterial sequences

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<220>  
<221> CDS  
<222> (1)..(1092)
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<400> 21  
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Met Ala Ile Ser Gly Val Pro Val Leu Gly Phe Phe Ile Ile Ala Val  
1 5 10 15

ctg atg agc gct cag gaa tca tgg gct atc aaa gaa gaa cat gtg atc	96
Leu Met Ser Ala Gln Glu Ser Trp Ala Ile Lys Glu Glu His Val Ile	
20 25 30	
atc cag gcc gag ttc tat ctg aat cct gac caa tca ggc gag ttt atg	144
Ile Gln Ala Glu Phe Tyr Leu Asn Pro Asp Gln Ser Gly Glu Phe Met	
35 40 45	
ttt gac ttt gat ggt gat gag att ttc cat gtg gat atg gca aag aag	192
Phe Asp Phe Asp Gly Asp Glu Ile Phe His Val Asp Met Ala Lys Lys	
50 55 60	
gag acg gtc tgg cgg ctt gaa gaa ttt gga cga ttt gcc agc ttt gag	240
Glu Thr Val Trp Arg Leu Glu Glu Phe Gly Arg Phe Ala Ser Phe Glu	
65 70 75 80	
gct caa ggt gca ttg gcc aac ata gct gtg gac aaa gcc aac ctg gaa	288
Ala Gln Gly Ala Leu Ala Asn Ile Ala Val Asp Lys Ala Asn Leu Glu	
85 90 95	
atc atg aca aag cgc tcc aac tat act ccg atc acc aat gta cct cca	336
Ile Met Thr Lys Arg Ser Asn Tyr Thr Pro Ile Thr Asn Val Pro Pro	
100 105 110	
gag gta act gtg ctc acg aac agc cct gtg gaa ctg aga gag ccc aac	384
Glu Val Thr Val Leu Thr Asn Ser Pro Val Glu Leu Arg Glu Pro Asn	
115 120 125	
gtc ctc atc tgt ttc atc gac aag ttc acc cca cca gtg gtc aat gtc	432
Val Leu Ile Cys Phe Ile Asp Lys Phe Thr Pro Pro Val Val Asn Val	
130 135 140	
acg tgg ctt cga aat gga aaa cct gtc acc aca gga gtg tca gag aca	480
Thr Trp Leu Arg Asn Gly Lys Pro Val Thr Thr Gly Val Ser Glu Thr	
145 150 155 160	
gtc ttc ctg ccc agg gaa gac cac ctt ttc cgc aag ttc cac tat ctc	528
Val Phe Leu Pro Arg Glu Asp His Leu Phe Arg Lys Phe His Tyr Leu	
165 170 175	
ccc ttc ctg ccc tca act gag gac gtt tac gac tgc agg gtg gag cac	576
Pro Phe Leu Pro Ser Thr Glu Asp Val Tyr Asp Cys Arg Val Glu His	
180 185 190	
tgg ggc ttg gat gag cct ctt ctc aag cac tgg gag ttt gat gct cca	624
Trp Gly Leu Asp Glu Pro Leu Leu Lys His Trp Glu Phe Asp Ala Pro	
195 200 205	
agc cct ctc cca gag act aca gag gaa ttc ggt ggt tcc ggt ggt tcc	672
Ser Pro Leu Pro Glu Thr Thr Glu Glu Phe Gly Gly Ser Gly Gly Ser	
210 215 220	
gcg cag ctg gaa tgg gaa ctg cag gcg ctg gaa aaa gaa aac gcg cag	720
Ala Gln Leu Glu Trp Glu Leu Gln Ala Leu Glu Lys Glu Asn Ala Gln	
225 230 235 240	

```

ctg gaa tgg gaa ctg cag gcg ctg gaa aaa gaa ctg gcg cag ggc ggc 768
Leu Glu Trp Glu Leu Gln Ala Leu Glu Lys Glu Leu Ala Gln Gly Gly
                245                250                255

tcc ggt ggt agc gcc aca cct caa aat att act gat ttg tgt gca gaa 816
Ser Gly Gly Ser Ala Thr Pro Gln Asn Ile Thr Asp Leu Cys Ala Glu
                260                265                270

tac cac aac aca caa ata cat acg cta aat gat aag ata ttt tcg tat 864
Tyr His Asn Thr Gln Ile His Thr Leu Asn Asp Lys Ile Phe Ser Tyr
                275                280                285

aca gaa tct cta gct gga aaa aga gag atg gct atc att act ttt aag 912
Thr Glu Ser Leu Ala Gly Lys Arg Glu Met Ala Ile Ile Thr Phe Lys
                290                295                300

aat ggt gca act ttt caa gta gaa gta cca ggt agt caa cat ata gat 960
Asn Gly Ala Thr Phe Gln Val Glu Val Pro Gly Ser Gln His Ile Asp
305                310                315                320

tca caa aaa aaa gcg att gaa agg atg aag gat acc ctg agg att gca 1008
Ser Gln Lys Lys Ala Ile Glu Arg Met Lys Asp Thr Leu Arg Ile Ala
                325                330                335

tat ctt act gaa gct aaa gtc gaa aag tta tgt gta tgg aat aat aaa 1056
Tyr Leu Thr Glu Ala Lys Val Glu Lys Leu Cys Val Trp Asn Asn Lys
                340                345                350

acg cct cat gcg att gcc gca att agt atg gca aat taa 1095
Thr Pro His Ala Ile Ala Ala Ile Ser Met Ala Asn
                355                360

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<210> 22

<211> 364

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fusion construct with human and bacterial sequences

<400> 22

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Met Ala Ile Ser Gly Val Pro Val Leu Gly Phe Phe Ile Ile Ala Val
 1                5                10                15

Leu Met Ser Ala Gln Glu Ser Trp Ala Ile Lys Glu Glu His Val Ile
                20                25                30

Ile Gln Ala Glu Phe Tyr Leu Asn Pro Asp Gln Ser Gly Glu Phe Met
                35                40                45

Phe Asp Phe Asp Gly Asp Glu Ile Phe His Val Asp Met Ala Lys Lys
50                55                60

Glu Thr Val Trp Arg Leu Glu Glu Phe Gly Arg Phe Ala Ser Phe Glu
65                70                75                80

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Ala	Gln	Gly	Ala	Leu	Ala	Asn	Ile	Ala	Val	Asp	Lys	Ala	Asn	Leu	Glu	
				85					90					95		
Ile	Met	Thr	Lys	Arg	Ser	Asn	Tyr	Thr	Pro	Ile	Thr	Asn	Val	Pro	Pro	
				100					105					110		
Glu	Val	Thr	Val	Leu	Thr	Asn	Ser	Pro	Val	Glu	Leu	Arg	Glu	Pro	Asn	
				115					120					125		
Val	Leu	Ile	Cys	Phe	Ile	Asp	Lys	Phe	Thr	Pro	Pro	Val	Val	Asn	Val	
				130					135					140		
Thr	Trp	Leu	Arg	Asn	Gly	Lys	Pro	Val	Thr	Thr	Gly	Val	Ser	Glu	Thr	
				145					150					155		
Val	Phe	Leu	Pro	Arg	Glu	Asp	His	Leu	Phe	Arg	Lys	Phe	His	Tyr	Leu	
				165					170					175		
Pro	Phe	Leu	Pro	Ser	Thr	Glu	Asp	Val	Tyr	Asp	Cys	Arg	Val	Glu	His	
				180					185					190		
Trp	Gly	Leu	Asp	Glu	Pro	Leu	Leu	Lys	His	Trp	Glu	Phe	Asp	Ala	Pro	
				195					200					205		
Ser	Pro	Leu	Pro	Glu	Thr	Thr	Glu	Glu	Phe	Gly	Gly	Ser	Gly	Gly	Ser	
				210					215					220		
Ala	Gln	Leu	Glu	Trp	Glu	Leu	Gln	Ala	Leu	Glu	Lys	Glu	Asn	Ala	Gln	
				225					230					235		
Leu	Glu	Trp	Glu	Leu	Gln	Ala	Leu	Glu	Lys	Glu	Leu	Ala	Gln	Gly	Gly	
				245					250					255		
Ser	Gly	Gly	Ser	Ala	Thr	Pro	Gln	Asn	Ile	Thr	Asp	Leu	Cys	Ala	Glu	
				260					265					270		
Tyr	His	Asn	Thr	Gln	Ile	His	Thr	Leu	Asn	Asp	Lys	Ile	Phe	Ser	Tyr	
				275					280					285		
Thr	Glu	Ser	Leu	Ala	Gly	Lys	Arg	Glu	Met	Ala	Ile	Ile	Thr	Phe	Lys	
				290					295					300		
Asn	Gly	Ala	Thr	Phe	Gln	Val	Glu	Val	Pro	Gly	Ser	Gln	His	Ile	Asp	
				305					310					315		
Ser	Gln	Lys	Lys	Ala	Ile	Glu	Arg	Met	Lys	Asp	Thr	Leu	Arg	Ile	Ala	
				325					330					335		
Tyr	Leu	Thr	Glu	Ala	Lys	Val	Glu	Lys	Leu	Cys	Val	Trp	Asn	Asn	Lys	
				340					345					350		
Thr	Pro	His	Ala	Ile	Ala	Ala	Ile	Ser	Met	Ala	Asn					
				355					360							

<210> 23  
 <211> 861  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fusion construct with human and bacterial sequences

<220>

<221> CDS

<222> (1)..(855)

<400> 23

atg	gtg	tgt	ctg	aag	ttc	cct	gga	ggc	tcc	tgc	atg	gca	gct	ctg	aca	48
Met	Val	Cys	Leu	Lys	Phe	Pro	Gly	Gly	Ser	Cys	Met	Ala	Ala	Leu	Thr	
1				5					10					15		
gtg	aca	ctg	atg	gtg	ctg	agc	tcc	cca	ctg	gct	ttg	gct	ggg	gac	acc	96
Val	Thr	Leu	Met	Val	Leu	Ser	Ser	Pro	Leu	Ala	Leu	Ala	Gly	Asp	Thr	
			20					25					30			
cga	cca	cgt	ttc	ttg	gag	cag	gtt	aaa	cat	gag	tgt	cat	ttc	ttc	aac	144
Arg	Pro	Arg	Phe	Leu	Glu	Gln	Val	Lys	His	Glu	Cys	His	Phe	Phe	Asn	
		35					40					45				
ggg	acg	gag	cgg	gtg	cgg	ttc	ctg	gac	aga	tac	ttc	tat	cac	caa	gag	192
Gly	Thr	Glu	Arg	Val	Arg	Phe	Leu	Asp	Arg	Tyr	Phe	Tyr	His	Gln	Glu	
	50					55				60						
gag	tac	gtg	cgc	ttc	gac	agc	gac	gtg	ggg	gag	tac	cgg	gcg	gtg	acg	240
Glu	Tyr	Val	Arg	Phe	Asp	Ser	Asp	Val	Gly	Glu	Tyr	Arg	Ala	Val	Thr	
	65				70					75					80	
gag	ctg	ggg	cgg	cct	gat	gcc	gag	tac	tgg	aac	agc	cag	aag	gac	ctc	288
Glu	Leu	Gly	Arg	Pro	Asp	Ala	Glu	Tyr	Trp	Asn	Ser	Gln	Lys	Asp	Leu	
				85					90					95		
ctg	gag	cag	aag	cgg	gcc	gcg	gtg	gac	acc	tac	tgc	aga	cac	aac	tac	336
Leu	Glu	Gln	Lys	Arg	Ala	Ala	Val	Asp	Thr	Tyr	Cys	Arg	His	Asn	Tyr	
			100					105					110			
ggg	gtt	ggt	gag	agc	ttc	aca	gtg	cag	cgg	cga	gtc	tat	cct	gag	gtg	384
Gly	Val	Gly	Glu	Ser	Phe	Thr	Val	Gln	Arg	Arg	Val	Tyr	Pro	Glu	Val	
	115						120					125				
act	gtg	tat	cct	gca	aag	acc	cag	ccc	ctg	cag	cac	cac	aac	ctc	ctg	432
Thr	Val	Tyr	Pro	Ala	Lys	Thr	Gln	Pro	Leu	Gln	His	His	Asn	Leu	Leu	
	130					135					140					
gtc	tgc	tct	gtg	aat	ggt	ttc	tat	cca	ggc	agc	att	gaa	gtc	agg	tgg	480
Val	Cys	Ser	Val	Asn	Gly	Phe	Tyr	Pro	Gly	Ser	Ile	Glu	Val	Arg	Trp	
	145				150					155					160	
ttc	cgg	aac	ggc	cag	gaa	gag	aag	act	ggg	gtg	gtg	tcc	aca	ggc	ctg	528
Phe	Arg	Asn	Gly	Gln	Glu	Glu	Lys	Thr	Gly	Val	Val	Ser	Thr	Gly	Leu	
				165					170					175		

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atc cag aat gga gac tgg acc ttc cag acc ctg gtg atg ctg gaa aca 576
Ile Gln Asn Gly Asp Trp Thr Phe Gln Thr Leu Val Met Leu Glu Thr
      180                      185                      190

gtt cct cgg agt gga gag gtt tac acc tgc caa gtg gag cac cca agc 624
Val Pro Arg Ser Gly Glu Val Tyr Thr Cys Gln Val Glu His Pro Ser
      195                      200                      205

ctg acg agc cct ctc aca gtg gaa tgg aga gca cgg tct gaa tct gca 672
Leu Thr Ser Pro Leu Thr Val Glu Trp Arg Ala Arg Ser Glu Ser Ala
      210                      215                      220

cag agc aag ggc ggc tcc ggt ggt agc gcc cag ctg aag aag aaa ctc 720
Gln Ser Lys Gly Gly Ser Gly Gly Ser Ala Gln Leu Lys Lys Lys Leu
      225                      230                      235                      240

cag gct ctg aaa aaa aag aat gcc cag ctc aag cag aag ctg cag gcc 768
Gln Ala Leu Lys Lys Lys Asn Ala Gln Leu Lys Gln Lys Leu Gln Ala
      245                      250                      255

ctg aag aaa aag ctg gct cag ggt tcc ggt ggt tcc gcg ggt ggt ggt 816
Leu Lys Lys Lys Leu Ala Gln Gly Ser Gly Gly Ser Ala Gly Gly Gly
      260                      265                      270

ttg aac gac atc ttc gaa gct cag aaa atc gaa tgg cac taataa 861
Leu Asn Asp Ile Phe Glu Ala Gln Lys Ile Glu Trp His
      275                      280                      285

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<210> 24

<211> 285

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fusion construct with human and bacterial sequences

<400> 24

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Met Val Cys Leu Lys Phe Pro Gly Gly Ser Cys Met Ala Ala Leu Thr
 1              5              10              15

Val Thr Leu Met Val Leu Ser Ser Pro Leu Ala Leu Ala Gly Asp Thr
      20              25              30

Arg Pro Arg Phe Leu Glu Gln Val Lys His Glu Cys His Phe Phe Asn
      35              40              45

Gly Thr Glu Arg Val Arg Phe Leu Asp Arg Tyr Phe Tyr His Gln Glu
      50              55              60

Glu Tyr Val Arg Phe Asp Ser Asp Val Gly Glu Tyr Arg Ala Val Thr
      65              70              75              80

Glu Leu Gly Arg Pro Asp Ala Glu Tyr Trp Asn Ser Gln Lys Asp Leu
      85              90              95

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Leu Glu Gln Lys Arg Ala Ala Val Asp Thr Tyr Cys Arg His Asn Tyr  
 100 105 110  
 Gly Val Gly Glu Ser Phe Thr Val Gln Arg Arg Val Tyr Pro Glu Val  
 115 120 125  
 Thr Val Tyr Pro Ala Lys Thr Gln Pro Leu Gln His His Asn Leu Leu  
 130 135 140  
 Val Cys Ser Val Asn Gly Phe Tyr Pro Gly Ser Ile Glu Val Arg Trp  
 145 150 155 160  
 Phe Arg Asn Gly Gln Glu Glu Lys Thr Gly Val Val Ser Thr Gly Leu  
 165 170 175  
 Ile Gln Asn Gly Asp Trp Thr Phe Gln Thr Leu Val Met Leu Glu Thr  
 180 185 190  
 Val Pro Arg Ser Gly Glu Val Tyr Thr Cys Gln Val Glu His Pro Ser  
 195 200 205  
 Leu Thr Ser Pro Leu Thr Val Glu Trp Arg Ala Arg Ser Glu Ser Ala  
 210 215 220  
 Gln Ser Lys Gly Gly Ser Gly Gly Ser Ala Gln Leu Lys Lys Lys Leu  
 225 230 235 240  
 Gln Ala Leu Lys Lys Lys Asn Ala Gln Leu Lys Gln Lys Leu Gln Ala  
 245 250 255  
 Leu Lys Lys Lys Leu Ala Gln Gly Ser Gly Gly Ser Ala Gly Gly Gly  
 260 265 270  
 Leu Asn Asp Ile Phe Glu Ala Gln Lys Ile Glu Trp His  
 275 280 285